

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2002, 21:05:33 : Search time 27 Seconds
(without alignments)
1480.068 Million cell updates/sec

Title: US-09-840-795-19
Perfect score: 1273
Sequence: 1 MDCQENEYWDQMGRCVTCOR.....AQLFSLDSVPIPPQGGGPEM 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | ID | Description |
|------------|-------|---------------|--------|----|-------------|
| 1 | 1132 | 88.9 | 297 | 4 | O9HAV5 |
| 2 | 485 | 38.1 | 423 | 4 | O9NZV2 |
| 3 | 483 | 37.9 | 417 | 4 | O9BY00 |
| 4 | 483 | 37.9 | 423 | 4 | O9NS68 |
| 5 | 480 | 37.7 | 423 | 4 | O9BX29 |
| 6 | 478 | 37.5 | 348 | 11 | O9QXW7 |
| 7 | 478 | 37.5 | 416 | 11 | O9J3H6 |
| 8 | 478 | 37.5 | 416 | 11 | O9J3H6 |
| 9 | 474 | 37.2 | 214 | 11 | O9JHFL |
| 10 | 406 | 31.9 | 150 | 11 | O9JILL2 |
| 11 | 199.5 | 15.7 | 448 | 4 | O9UNE0 |
| 12 | 192.5 | 15.1 | 448 | 4 | O9UND9 |
| 13 | 183.5 | 13.4 | 448 | 4 | O9R187 |
| 14 | 166.5 | 13.1 | 514 | 13 | O9OVY2 |
| 15 | 164.5 | 12.9 | 514 | 13 | O9O236 |
| 16 | 157.5 | 12.4 | 186 | 12 | O911R5 |

| | | | | | | |
|----|-------|------|-----|----|--------|---------------------|
| 17 | 156.5 | 12.3 | 186 | 12 | O72735 | cowpox viru |
| 18 | 153.5 | 12.1 | 186 | 12 | O9WJB4 | 09wbj4 vaccinia vi |
| 19 | 150.5 | 11.8 | 186 | 12 | O9YP87 | 09yp87 cowpox viru |
| 20 | 148 | 11.6 | 438 | 13 | O9DFV0 | 09dfv0 brachydanio |
| 21 | 145.5 | 11.4 | 276 | 13 | O9DD02 | 09dd02 gallus gall |
| 22 | 145 | 11.4 | 283 | 6 | O9XS28 | 09xs28 cercopithe |
| 23 | 143.5 | 11.3 | 430 | 6 | O9N092 | 09n092 macaca fasc |
| 24 | 141.5 | 11.1 | 283 | 4 | O96J31 | 096j31 homo sapien |
| 25 | 141 | 11.1 | 302 | 13 | O9PUS0 | 09pus0 salvelinus |
| 26 | 140.5 | 11.0 | 175 | 12 | O9PZR3 | 09pzr3 human cytom |
| 27 | 140.5 | 11.0 | 430 | 4 | O96J01 | 096j01 homo sapien |
| 28 | 140.5 | 11.0 | 430 | 4 | O96924 | 096924 homo sapien |
| 29 | 137.5 | 10.8 | 327 | 6 | O97491 | 097491 ovis aries |
| 30 | 137 | 10.8 | 350 | 12 | O57116 | 057116 cowpox viru |
| 31 | 135.5 | 10.6 | 175 | 12 | O9PZS0 | 09pzs0 human cytom |
| 32 | 135.5 | 10.6 | 347 | 12 | O57115 | 057115 cowpox viru |
| 33 | 133 | 10.4 | 176 | 12 | O9PZR2 | 09pzr2 human cytom |
| 34 | 133 | 10.4 | 387 | 13 | O9PYD4 | 09pyd4 xenopus lae |
| 35 | 132.5 | 10.4 | 349 | 12 | O57305 | 057305 cowpox viru |
| 36 | 132.5 | 10.4 | 355 | 12 | O85308 | 085308 unidentified |
| 37 | 132.5 | 10.4 | 425 | 4 | O16042 | O16042 homo sapien |
| 38 | 132 | 10.4 | 176 | 12 | O9PZR8 | 09pzr8 human cytom |
| 39 | 131 | 10.3 | 433 | 11 | O912M6 | 0912m6 rattus norv |
| 40 | 131 | 10.3 | 461 | 11 | O91V30 | 091v30 rattus norv |
| 41 | 130 | 10.2 | 176 | 12 | O9PZR9 | 09pzr9 human cytom |
| 42 | 130 | 10.2 | 461 | 11 | O91Y93 | 091y93 rattus norv |
| 43 | 129.5 | 10.2 | 327 | 11 | O9DCQ1 | 09dcq1 mus musculu |
| 44 | 129.5 | 10.2 | 331 | 6 | O9TSM4 | 09tsm4 macaca fasc |
| 45 | 129.5 | 10.2 | 331 | 6 | O9BDN0 | 09bdn0 macaca neme |

ALIGNMENTS

RESULT 1

ID O9HAV5 PRELIMINARY; PRT; 297 AA.
AC O9HAV5:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE X-LINKED ECTODYSPLASIN-A2 RECEPTOR.
GN XEDAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP
RX MEDLINE=20495245; PubMed=11039935;
RA Yan M., Wang L.C., Hymowitz S.G., Schilbach S., Lee J., Goddard A.,
RA de Vos A.M., Gao W.Q., Dixit V.M.;
RT "Two-amino acid molecular switch in an epithelial morphogen that
RT regulates binding to two distinct receptors.";
RL Science 290:523-527(2000).
DR EMBL: AF298812; AAC28761.1; -
DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF00020; TNFR_C6; 2.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS00505; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 297 AA; 32728 MW; DE71127C6C48240C CRC64;
Query Match 88.9%; Score 1132; DB 4; Length 297;
Best Local Similarity 99.5%; Pred. No. 4,7e-114;
Matches 204; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 MDCQENEYWDQMGRCVTCORCGPQGLSKDCGYGBGDATCTACPPRYKSKWGHKQCS 60
|||||
DB 1 MDCQENEYWDQMGRCVTCORCGPQGLSKDCGYGBGDATCTACPPRYKSKWGHKQCS 60
|||||
OY 61 CITCAVINRQVKVNCATATSNVCGDCLPRFYRKTRIGSLQDQECIPCKKPTSTVEYQCAF 120

```

Db 61 CITCAVINRQKVCATATSNVAGDCLPRFYRKTRIGLQDOECIPCTKQPTSEVQCAF 120
OY 121 QLSLVEADAPVPPQENATVALVSSLLVFTLAFGLFLFYCKQFNRHRCQRGGLQFEA 180
Db 121 QLSLVEADAPVPPQENATVALVSSLLVFTLAFGLFLFYCKQFNRHRCQRGGLQFEA 180
OY 181 DKTAKESLFPVPPSKETSASQVS 205
Db 181 DKTAKESLFPVPPSKETSASQVS 205

```

RESULT 2

```

O9NZV2 PRELIMINARY; PRT; 423 AA.

```

```

AC O9NZV2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE TAJ-ALPHA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20270246; PubMed=10809768;
RA Eby M.T., Jasmán A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
RT Independent Cell Death.";
RL J. Biol. Chem. 275:15336-15342(2000).
DR EMBL; AF167555; AAF71828.1; -.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 423 AA; 46071 MW; BB7C9917132A4B2F CRC64;

```

```

Query Match 38.1%; Score 485; DB 4; Length 423;
Best Local Similarity 44.9%; Pred. No. 5e-44;
Matches 88; Conservative 29; Mismatches 79; Indels 0; Gaps 0;

```

```

OY 2 DCOENYWDQRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSMGHHKQSC 61
Db 33 DCRQOEFRRSGNCVPCNCGGFMELSKDCGFYGEDACVCTRLHREKEDWGFGCKPC 92
OY 62 ITCAVINRQKVCATATSNVAGDCLPRFYRKTRIGLQDOECIPCTKQPTSEVQCAF 121
Db 93 LDCAVNRFQKANCSTSDALIGDCLPGFYRKTKLVGFQDMCVCPGDPPEYEPHCASK 152
OY 122 LSLVEADAPVPPQENATVALVSSLLVFTLAFGLFLFYCKQFNRHRCQRGGLQFEAD 181
Db 153 VNLVRIASPRDTALAIVCSALATVLLILICVYICKRQPMKKPSMSLSQDIO 212
OY 182 KTKAKESLFPVPPSKE 197
Db 213 YNTELSGCFDRQLHE 228

```

RESULT 3

```

O9BY00 PRELIMINARY; PRT; 417 AA.

```

```

AC O9BY00;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-OCT-2001 (TREMBlrel. 16, Last annotation update)
DE TRDEALPHA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RA Chaudhary D., Long A.J.;
RT "TRADE, a novel TNF receptor family member associated with death
RT signaling.";
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF246998; AAK28395.1; -.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 417 AA; 45319 MW; 3AA85D7827AB35C4 CRC64;

```

```

Query Match 37.9%; Score 483; DB 4; Length 417;
Best Local Similarity 44.4%; Pred. No. 8.1e-44;
Matches 87; Conservative 29; Mismatches 80; Indels 0; Gaps 0;

```

```

OY 2 DCOENYWDQRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSMGHHKQSC 61
Db 33 DCRQOEFRRSGNCVPCNCGGFMELSKDCGFYGEDACVCTRLHREKEDWGFGCKPC 92
OY 62 ITCAVINRQKVCATATSNVAGDCLPRFYRKTRIGLQDOECIPCTKQPTSEVQCAF 121
Db 93 LDCAVNRFQKANCSTSDALIGDCLPGFYRKTKLVGFQDMCVCPGDPPEYEPHCASK 152
OY 122 LSLVEADAPVPPQENATVALVSSLLVFTLAFGLFLFYCKQFNRHRCQRGGLQFEAD 181
Db 153 VNLVRIASPRDTALAIVCSALATVLLILICVYICKRQPMKKPSMSLSQDIO 212
OY 182 KTKAKESLFPVPPSKE 197
Db 213 YNTELSGCFDRQLHE 228

```

RESULT 4

```

O9NS68 PRELIMINARY; PRT; 423 AA.

```

```

AC O9NS68;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HTROY.
GN HTROY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20347167; PubMed=10764796;
RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Senba E., Kitamura T.;
RT "HTROY, a newly identified member of the tumor necrosis factor receptor
RT superfamily, exhibits a homology with Edar and is expressed in
RT embryonic skin and hair follicles.";
RL J. Biol. Chem. 275:20742-20747(2000).
DR EMBL; AB040434; BAB03269.1; -.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 423 AA; 46015 MW; B5891CEA9ED45361 CRC64;

```

```

Query Match 37.9%; Score 483; DB 4; Length 423;
Best Local Similarity 44.4%; Pred. No. 8.2e-44;
Matches 87; Conservative 29; Mismatches 80; Indels 0; Gaps 0;

```

```

OY 2 DCOENYWDQRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSMGHHKQSC 61
Db 33 DCRQOEFRRSGNCVPCNCGGFMELSKDCGFYGEDACVCTRLHREKEDWGFGCKPC 92

```

```

QY  ITCVIRRVQVNTATFASNAVCDCLPFRKTRIGLDOECJPCTKQMPFSVQCFAFQ 121
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  LDCAVVRNFQKANC SATSDACGCGCLCEGFYKRTKLVBFQDMCECPDPPEYPFHASK 152
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  LSLVEADAPVPPOEATLVALVSLVFTLAFGLFELYCKQGFENHCQRGSLGFEAD 181
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  VNLVKIAISTASSPDOTMLAAVICALATVLTALLILCIVYCKQFMKKPMSWLSRSODIQ 212
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  KTAKEESLFPVPSPSKE 197
    | | | | |
Db  YNGSELSCFDRPOLHE 228
    | | | | |

```

| RESULT 5 | Q9BXZ9 | PRELIMINARY; | PRT; | 423 AA. |
|----------|--|--------------|------|---------|
| AC | Q9BXZ9; | | | |
| DT | 01-JUN-2001 (TREMBLrel. 17, Created) | | | |
| DT | 01-JUN-2001 (TREMBLrel. 17, last sequence update) | | | |
| DT | 01-OCT-2001 (TREMBLrel. 18, last annotation update) | | | |
| DE | TRADEBERTA. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxId=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Chaudhary D., Long A.J.; | | | |
| RT | "TRADE, a novel TNF receptor family member associated with death | | | |
| RT | signaling". | | | |
| RL | Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases. | | | |
| DR | EMBL: AF246999; AKK28396.1; - | | | |
| DR | InterPro: IPR001368; TNFR_C6. | | | |
| DR | Pfam: PF00020; TNFR_C6; 2. | | | |
| DR | SMART: SM00208; TNFR: 2. | | | |
| DR | PROSITE: PS00652; TNFR_NGFR.1; UNKNOWN.2. | | | |
| DR | PROSITE: PS50050; TNFR_NGFR.2; 1. | | | |
| QO | SEQUENCE 423 AA; 45979 MW; 44605641A8A96BA2 CRC64; | | | |

| | Query Match | 37.7% | Score 480 | DB 43 | Length 423 |
|----|-----------------------|--|-------------------|----------|------------|
| | Best Local Similarity | 49.1% | Pred. No. 1.7e+43 | | |
| | Matches 81 | Conservative 28 | Mismatches 56 | Indels 0 | Gaps 0 |
| Qy | 2 | DCQENRYWDQMGRCVTCORCGPGDELTKSDCGEGEGDGYCTCAPPRRYKSSVGHGHCOSC | 61 | | |
| Db | 33 | DCRQGFEEFRDRGNCVPCPCQCGCGMELSKDECGFGYEDDQCVTYCRHLRRFREDDMGFOCKRC | 92 | | |
| Qy | 62 | ITCAVINRQKVNCTATISNAVCGDCLPRFYRRTIRIGLQDDECIPCTKOTPTSEVQCAFO | 121 | | |
| Db | 93 | LDCAVVNRFRQKANCATSATSDAICGDCLPGFYRRTKTLVGFQDMCVCPCGDPPEPYEPhCASK | 152 | | |
| Qy | 122 | LSLVEADAPVTPQDEATLVAVSSLLVYFTLAFGLGLFLYCKQFF | 166 | | |
| Db | 153 | VNLKIAISTASSPRDIALAIVICSLATLVALLLILCYICKRPF | 197 | | |

| RESULT | 6 |
|--------|---|
| 090XW7 | |
| ID | 090XW7 |
| AC | 090XW7; |
| DT | 01-MAY-2000 (TREMBLrel. 13, Created) |
| DT | 01-MAY-2000 (TREMBLrel. 13, Last sequence update) |
| DT | 01-JUN-2001 (TREMBLrel. 17, Last annotation update) |
| DE | TREBSF19. |
| GN | TREBSF19. |
| OS | Mus musculus (Mouse). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus |
| OX | NCBI_Taxid-10090; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RX | MEDLINE-20054362; PubMed-10585776; |
| RA | Hu S., Yamada K., Ni J., Vincenz C., Chen L.; |

RT "characterization of TNFSF19, a novel member of tumor necrosis factor receptor superfamily." ;

RL Genomics 62:103-107(1999).

DR EMBL: AF173166; AAF19795.1; -

DR MGD: MGI:1352474; Tnfstf19.

DR InterPro: IPR001368; TNFR_C6.

DR Pfam: PF00020; TNFR_C6; 2.

DR SMART: SM00208; TNFR; 2.

DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_2.

DR PROSITE: PS00650; TNFR_NGFR_2; 1.

SO SEQUENCE 348 AA; 38450 MW; 013C799638FB8333 CRC64;

| | | | | | | |
|----|---|------------------|---------------------|------------|-------------|--|
| | Query Match | 37.5%; | Score 478; | D8 11; | Length 348; | |
| | Best Local Similarity | 40.4%; | Pred. No. 2, 3e-43; | | | |
| | Matches 84; | Conservative 30; | Mismatches 66; | Indels 28; | Gaps | |
| QY | 2 DCOENEXWDMGRVCVTCORCGPGGELS KDCGYEGGDATYCTACPRRYKSSWGHNKSC | 61 | | | | |
| | : : : : : : : | | | | | |
| D8 | 33 DCROEFKRDRSGNVLCKOCGPMELSKECGFGEADAOCPVRPNHFKEDMFGOKPC | 92 | | | | |
| QY | 62 ITCAVIRVQKVNCTATSNMGDGLCFRPFRTKPIIGLDOECIPCTKHQTSEVGCAPQ | 121 | | | | |
| | : : : : : : | | | | | |
| D8 | 93 ADCALVNRFORANCSHTSDAAGDCLGFTFRKTQLVGFOIMECVPCGDDPPPEPHCTSK | 152 | | | | |
| QY | 122 LSLVEADAPTVPQEATLVALLVSSLVAVFTLAFLGTFLLYKCOFFN----- | 167 | | | | |
| | : : : : : : : : : : : : : : : : : : | | | | | |
| D8 | 153 VNLVKISSTVSSPRDATALAAVTICALATLVALLILICVIYCKQFMKKRFSWSLRPDQI | 212 | | | | |
| QY | 168 -----RHCRGGSLDGFEND 181 | | | | | |
| | : : : | | | | | |
| D8 | 213 YNGSELSCFDOPRLRHCAHRACCQYHRD 240 | | | | | |

| | | | |
|---|--------------|------------|--------------------|
| RESULT 7 | | | |
| 09JUH6 | PRELIMINARY; | PRT; | 416 AA. |
| ID 09JUH6 | | | |
| AC 09JUH6; | | | |
| DT 01-OCT-2000 (TReMBLrel. 15, Created) | | | |
| DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update) | | | |
| DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update) | | | |
| DE TROY (TRADE). | | | |
| GN TNRSF19 OR TROY. | | | |
| OS Mus musculus (Mouse). | | | |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX NCBI_TaxID=10090; | | | |
| RN [1] | | | |
| RP SEQUENCE FROM N.A. | | | |
| RX MEDLINE=20347167; PubMed=10764796; | | | |
| RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A., | | | |
| RA Senba E., Kitamura T., | | | |
| RT "TROY, a newly identified member of the tumor necrosis factor receptor | | | |
| RT superfamily, exhibits a homology with Edar and is expressed in | | | |
| RT embryonic skin and hair follicles."; | | | |
| RL J. Biol. Chem. 275:20742-20747(2000). | | | |
| RN [2] | | | |
| RP SEQUENCE FROM N.A. | | | |
| RC STRAIN=C57BL/6; | | | |
| RA Chaughary D., Long A.J.; | | | |
| RT "RRAD6, a novel TNF receptor family member associated with death | | | |
| RT signaling," | | | |
| RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases. | | | |
| DR EMBL: AB040432; BAB03267.1; - | | | |
| DR EMBL: AF247000; AAK28397.1; - | | | |
| DR MGD: MGI:1352474; Tnfrsf19. | | | |
| DR InterPro: IPR001368; TNRFC6. | | | |
| DR Pfam: PF000020; TNRFC6; 2. | | | |
| DR SMART: SM00208; TNRFC6; 2. | | | |
| DR PROSITE: PS00652; TNR_NGFR_1; UNKNOWN_2. | | | |
| DR PROSITE: PS50050; TNR_NGFR_2; 1. | | | |
| DR SEQUENCE 416 AA; 45265 MW; 9B9C7CA2D6A9C47 CRC64; | | | |
| Query Match | 37.5%; | Score 478; | DB 11; Length 416; |

Best Local Similarity 40.4%; Pred. No. 2.8e-43;
Matches 84; Conservative 30; Mismatches 66; Indels 28; Gaps 1;

OY 2 DCOENEMYDQMGRCVTCORCGPQELSKDCGYEGGDAYTACPPRRYKSSGHHKQSC 61
DB 33 DCRQEFKDRSGNVCVLCQCGPQELSKDCGYEGGDAYTACPPRRYKSSGHHKQSC 92
OY 62 ITCAVINRVQKVNCTATSNVAGDCLPFRYKTRIGLQDECIPTCKQPTSEVOCARQ 121
DB 93 ADCALVNRQFQANCSTSDAVCGDCLPFRYKTRIGLQDECIPTCKQPTSEVOCARQ 152
OY 122 LSLVEADAPVPPOEATLVALVSSLLVFTLAFGLFPLYCKQFNN----- 167
DB 153 VNLVKISSTVSSPRDTALAIVCSALATVLLILLCVICYCKRQFMKKRPSWLSRSDIQ 212
OY 168 -----RHQGRGLQFEAD 181
DB 213 YNGSELSCFDQPRRLRHAHRACQYHRD 240

RESULT 8

OYJUL3 PRELIMINARY; PRT; 416 AA.
AC 09JUL3
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TAJ-ALPHA LONG.
GN TNRFSF19.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20270246; PubMed=10809768;
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
RL J. Biol. Chem. 275:15336-15342(2000).
DR EMBL; AF167552; AAF71825.1;
DR MGI; MGI:1352474; Tnfrsf19.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00202; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00650; TNFR_NGFR_2; 1.
SQ SEQUENCE 416 AA; 45294 MM; 19CA2F75DD7B9D49 CRC64;

Query Match 37.5%; Score 478; DB 11; Length 416;
Best Local Similarity 40.4%; Pred. No. 2.8e-43;
Matches 84; Conservative 30; Mismatches 66; Indels 28; Gaps 1;

OY 2 DCOENEMYDQMGRCVTCORCGPQELSKDCGYEGGDAYTACPPRRYKSSGHHKQSC 61
DB 33 DCRQEFKDRSGNVCVLCQCGPQELSKDCGYEGGDAYTACPPRRYKSSGHHKQSC 92
OY 62 ITCAVINRVQKVNCTATSNVAGDCLPFRYKTRIGLQDECIPTCKQPTSEVOCARQ 121
DB 93 ADCALVNRQFQANCSTSDAVCGDCLPFRYKTRIGLQDECIPTCKQPTSEVOCARQ 152
OY 122 LSLVEADAPVPPOEATLVALVSSLLVFTLAFGLFPLYCKQFNN----- 167
DB 153 VNLVKISSTVSSPRDTALAIVCSALATVLLILLCVICYCKRQFMKKRPSWLSRSDIQ 212
OY 168 -----RHQGRGLQFEAD 181
DB 213 YNGSELSCFDQPRRLRHAHRACQYHRD 240

RESULT 9

OYJUL3

ID 09JUL3 PRELIMINARY; PRT; 214 AA.
AC 09JUL3
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DTROY (TAJ-ALPHA SHORT).
GN TNRFSF19 OR DTROY.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20347167; PubMed=10764796;
RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Senba E., Kitamura T.;
RT "TRDY, a newly identified member of the tumor necrosis factor receptor
RT superfamily, exhibits a homology with Edar and is expressed in
RT embryonic skin and hair follicles";
RL J. Biol. Chem. 275:20742-20747(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20270246; PubMed=10809768;
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
RL J. Biol. Chem. 275:15336-15342(2000).
DR EMBL; AB040433; BAB03268.1;
DR EMBL; AF167553; AAF71826.1;
DR MGI; MGI:1352474; Tnfrsf19.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00202; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00650; TNFR_NGFR_2; 1.
SQ SEQUENCE 214 AA; 23564 MM; ECC63981C37482B8 CRC64;

Query Match 37.2%; Score 474; DB 11; Length 214;
Best Local Similarity 47.9%; Pred. No. 3.6e-43;
Matches 79; Conservative 29; Mismatches 57; Indels 0; Gaps 0;

OY 2 DCOENEMYDQMGRCVTCORCGPQELSKDCGYEGGDAYTACPPRRYKSSGHHKQSC 61
DB 33 DCRQEFKDRSGNVCVLCQCGPQELSKDCGYEGGDAYTACPPRRYKSSGHHKQSC 92
OY 62 ITCAVINRVQKVNCTATSNVAGDCLPFRYKTRIGLQDECIPTCKQPTSEVOCARQ 121
DB 93 ADCALVNRQFQANCSTSDAVCGDCLPFRYKTRIGLQDECIPTCKQPTSEVOCARQ 152
OY 122 LSLVEADAPVPPOEATLVALVSSLLVFTLAFGLFPLYCKQFNN----- 166
DB 153 VNLVKISSTVSSPRDTALAIVCSALATVLLILLCVICYCKRQF 197

RESULT 10
OYJUL2 PRELIMINARY; PRT; 150 AA.
AC 09JUL2
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TAJ-BETA1.
GN TNRFSF19.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20270246; PubMed=10809768;
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,

RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
RT Independent Cell Death."
RL J. Biol. Chem. 275:15336-15342(2000).
DR EMBL: AF167554; AAF71827.1; -
DR MGD: MGI:1352474; Tnfrsf19.
DR InterPro: IPR001368; TNFR_c6.
DR SMART: SM00208; TNFR_c6; 2.
DR Pfam: PF00020; TNFR_c6; 2.
DR PROSITE: PS00652; TNFR_NGFR.1; UNKNOWN_2.
DR PROSITE: PS00650; TNFR_NGFR.2; 1.
SO SEQUENCE 150 AA; 16728 MW; 4A1B2E93AE7FE43 CRC64;

Query Match 31.9%; Score 406; DB 11; Length 150;
Best Local Similarity 54.7%; Pred. No. 5.3e-36;
Matches 64; Conservative 18; Mismatches 35; Indels 0; Gaps 0;

QY 2 DCOENEYWDQWGRVCYQRCRGPGQELSKDCGYEGGDAYCTACPPRRKXSSWGHKQSC 61
DB 33 DCRQGERDRKNCVILKQCGPMELSKCGYGEDACVPCRPKRREKEDMGFOCKKPC 92
QY 62 ITCVAVIRVOKNCTATSNVAVCGDCLPFRYKRTIGLQDOECJPTKQPTSEVQC 118
DB 93 ADCALVNRFORANCSSHSDAVCGDCLGFTYKTKLVGFQDMECVPCGDPPEPPYEPHC 149

RESULT 11

09UNE0 PRELIMINARY; PRT; 448 AA.
ID 09UNE0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 13, Last annotation update)
DE ECTODYSPLASIN-A RECEPTOR PROTEIN.
GN EDAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99364416; PubMed=10431241;
RA Montreal A.W., Ferguson B.M., Headon D.J., Street S.L., Overbeek P.A.,
RA Zonana J.;
RT "Mutations in the human homologue of mouse dl cause autosomal
RT recessive and dominant hypohidrotic ectodermal dysplasia.";
RL Nat. Genet. 22:366-369(1999).
DR EMBL: AF130988; AAD50076.1; -
DR HSSP: P25942; ICDF.
DR InterPro: IPR000488; Death.
DR Pfam: PF00531; death; 1.
KW Receptor.

SO SEQUENCE 448 AA; 48582 MW; AC8D61249D608439 CRC64;
Query Match 15.7%; Score 199.5; DB 4; Length 448;
Best Local Similarity 24.9%; Pred. No. 3.6e-13;
Matches 71; Conservative 33; Mismatches 112; Indels 69; Gaps 14;

QY 2 DCOENEYWDQWGRVCYQRCRGPGQELSKDCGYEGGDAYCTACPPRRKXSSWGHKQSC 54
DB 30 NCGENYNNQTTGLCQCCPPCGPEEPYLSGCGYCTKDEDCVPCPAKFSKGGYQICRR 89
QY 55 HHKQSCITTCVAVIRVOKNCTATSNVAVCGDCLPFRYKRTIGLQDOECJPTKQPT 113
DB 90 HKDCGFFRATVILPQGMEN-----DAECGCLPFGYMLNRPNNITGMVCYSCLLAPN 144
QY 114 SEVQCAFQSLVEADAP-----TVVPOE-----ATLVAVSSLLVFTLAFL 155
DB 145 TK-ECVATSGASANFPQTSSSTLSPQHNKELSGGHLATLITAMSTIFIMATAIV 203
QY 156 GLPFLY-----CKQFNNHCORGLQLEADTKAKE-----ESLF 190
DB 204 LIIMEYILKTRKPSAPACC-----TSHPGKSYEAQVSKDEKKEADPNVVFSEKDEFKEL- 258

QY 191 PVPSKETSASQSVSWAPGSLAQLFS-----LDSVPIPOOQOQPEM 231
DB 259 TATPAKPKTKSENDAS-----SENQILSRVSDSDDEPAPDKQSSPEL 300

RESULT 12

09UND9 PRELIMINARY; PRT; 448 AA.
ID 09UND9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ECTODYSPLASIN-A RECEPTOR PROTEIN.
GN EDAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99364416; PubMed=10431241;
RA Montreal A.W., Ferguson B.M., Headon D.J., Street S.L., Overbeek P.A.,
RA Zonana J.;
RT "Mutations in the human homologue of mouse dl cause autosomal
RT recessive and dominant hypohidrotic ectodermal dysplasia.";
RL Nat. Genet. 22:366-369(1999).
DR EMBL: AF130986; AAD50077.1; -
DR EMBL: AF130990; AAD50077.1; JOINED.
DR EMBL: AF130991; AAD50077.1; JOINED.
DR EMBL: AF130992; AAD50077.1; JOINED.
DR EMBL: AF130993; AAD50077.1; JOINED.
DR EMBL: AF130994; AAD50077.1; JOINED.
DR EMBL: AF130995; AAD50077.1; JOINED.
DR HSSP: P25942; ICDF.
DR InterPro: IPR000488; Death.
DR Pfam: PF00531; death; 1.
KW Receptor.

SO SEQUENCE 448 AA; 48572 MW; AC8E80F79CB255EA CRC64;

Query Match 15.1%; Score 192.5; DB 4; Length 448;
Best Local Similarity 23.1%; Pred. No. 2e-12;
Matches 66; Conservative 36; Mismatches 113; Indels 71; Gaps 12;

QY 2 DCOENEYWDQWGRVCYQRCRGPGQELSKDCGYEGGDAYCTACPPRRKXSSWGHKQSC 54
DB 30 NCGENYNNQTTGLCQCCPPCGPEEPYLSGCGYCTKDEDCVPCPAKFSKGGYQICRR 89
QY 55 HHKQSCITTCVAVIRVOKNCTATSNVAVCGDCLPFRYKRTIGLQDOECJPTKQPT 113
DB 90 HKDCGFFRATVILPQGMEN-----DAECGCLPFGYMLNRPNNITGMVCYSCLLAPN 144
QY 114 SEVQCAFQSLVEADAP-----TVVPOE-----ATLVAVSSLLVFTLAFL 155
DB 145 TK-ECVATSGASANFPQTSSSTLSPQHNKELSGGHLATLITAMSTIFIMATAIV 203
QY 156 GLPFLY-----CKQFNNHCORGLQLEADTKAKE-----ESLF 186
DB 204 LIIMEYILKTRKPSAPACC-----TSHPGKSYEAQVSKDEKKEADPNVVFSEKDEFKEL 259

RESULT 13

09RI87 PRELIMINARY; PRT; 448 AA.
ID 09RI87;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ECTODERMAL DYSPLASIA RECEPTOR.
GN EDAR OR DL.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9364417; PubMed=10431242;
 RA Headon D.J., Overbeek P.A.;
 RT "Involvement of a novel Tnf receptor homologue in hair follicle
 induction.";
 RL Nat. Genet. 22:370-374 (1999).
 DR EMBL: AF160502; AAD50425.1; -
 DR MGD: MGI:1343498; Edat.
 DR InterPro: IPR000488; Death.
 DR Pfam: PF00531; death; 1.
 KW Receptor.
 SQ SEQUENCE 448 AA; 48434 MW; FCCAF38F3D6B971 CRC64;

Query Match 14.4%; Score 183.5; DB 11; Length 448;
 Best Local Similarity 25.0%; Pred. No. 1.9e-11;
 Matches 70; Conservative 29; Mismatches 122; Indels 59; Gaps 13;

OY 2 DCOENYWDQGR-CVTCQRCGPQGLSKDCGYGEGGDAY-CTACPPRRY-----YKSSWG 54
 DB 30 NCGENETHMTGLCCQCPRCRGEPEYKSCGYGTDDDGVCVCPAEKFSKSGYICRR 89
 OY 55 HHKQGCITCAVINRQKNCATSNVAVGDCCLPRFYR-KTRIGGLQDDECIPTKQTPR 113
 DB 90 HKDCGEFFRATVLPQDMEN-----DAEGCPCLPGYMLERNRNIYGMVCSCLAPPR 144
 OY 114 SEVQCAFQSLVEADA-----FTVPPOE-----ATLVALVSSLVFTLAF 155
 DB 145 TK-ECVAGATSGVAHSSSTSGSTLSPFQAHKELSGQCHLATALIYAMSTIFMAIAY 203
 OY 156 GLEFLY-----CKQPFNRHCOGGLQFEADTKAKES-----LPP-----VPPS 195
 DB 204 LIIMFYIMKTKPSAPACSSPPKSKAEAPANTHEKKKEAPDSVVTTPPENGEFOKLTATPT 263
 OY 196 KETSAASQVSWAPGSLAQFS----IDSVPIPOQGGQPEM 231
 DB 264 KTRPSNDAS---SENEQLLSRSVSDDEPAPDKQGSPEL 300

RESULT 14
 O90VY2 PRELIMINARY; PRT; 514 AA.
 AC O90VY2;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ECTODYSPLASIN-A RECEPTOR.
 GN EDAR.
 OS Oryzias latipes (Medaka fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.
 ON NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RS-3, AND AA2;
 RA Kondo S., Shima A.;
 RT "The medaka rs-3 locus required for scale development encodes
 ectodysplasin-A receptor.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF364816; AAK83299.1; -
 DR EMBL: AF364814; AAK83297.1; -
 KW Receptor.
 SQ SEQUENCE 514 AA; 56066 MW; 82C7F0661EECFB48 CRC64;

Query Match 13.1%; Score 166.5; DB 13; Length 514;
 Best Local Similarity 24.5%; Pred. No. 1.5e-09;
 Matches 54; Conservative 38; Mismatches 101; Indels 27; Gaps 9;

OY 3 COENYWDQGR-CVTCQRCGPQGLSKDCGYGEGGDAY-CTACPPRRYKSSMGHHKOS 60
 DB 32 CGEYEFFNQTNSCOACPCQCRPGQEPNMSCGHMKDEGFAVCVPCPGKY-SKGYEICRR 90
 OY 61 CITC-AVINRQKNCATSNVAVGDCCLPRFYR-KTRIGGLQDDECIPTKQTPSEYOC 118
 DB 91 HKCQNALYKATVAREPQTAKDAECGCLGTGYMLENRANLIYAMVCHSC-QNAPLNTKEC 149
 OY 119 -----AFQSLVEADAPVYPO-----EATLVALVSSLVFTLAFGLFELYCK 163
 DB 150 KKTTEAITKPIIPNGSTTVLPHPGSPQCHLATALIYAMSTIFMAIAYLIMFYILKA 209
 OY 164 QFENRHCQGGILQFEADTKAKESLFYR-----PSKE 197
 DB 210 KPNGQACSGGVAVKAVEAQTNRKLEDKRDVDPNVVIFPEKE 249

RESULT 15
 O90Z36 PRELIMINARY; PRT; 514 AA.
 AC O90Z36;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ECTODYSPLASIN-A RECEPTOR.
 GN EDAR.
 OS Oryzias latipes (Medaka fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.
 ON NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HNT;
 RA Kondo S., Shima A.;
 RT "The medaka rs-3 locus required for scale development encodes
 ectodysplasin-A receptor.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF364815; AAK83298.1; -
 KW Receptor.
 SQ SEQUENCE 514 AA; 56074 MW; 8389E28082798632 CRC64;

Query Match 12.9%; Score 164.5; DB 13; Length 514;
 Best Local Similarity 25.5%; Pred. No. 2.5e-09;
 Matches 56; Conservative 34; Mismatches 103; Indels 27; Gaps 9;

OY 3 COENYWDQGR-CVTCQRCGPQGLSKDCGYGEGGDAY-CTACPPRRYKSSMGHHKOS 60
 DB 32 CGEYEFFNQTNSCOACPCQCRPGQEPNMSCGHMKDEGFAVCVPCPGKY-SKGYEICRR 90
 OY 61 CITC-AVINRQKNCATSNVAVGDCCLPRFYR-KTRIGGLQDDECIPTKQTPSEYOC 118
 DB 91 HKCQNALYKATVAREPQTAKDAECGCLGTGYMLENRANLIYAMVCHSC-QNAPLNTKEC 149
 OY 119 AFQSLVEADAPVYPOEATLVALVSSLVFTLA-----FLGFLFYLYCK 163
 DB 150 KKTTEAITKPIIPNGSTTVLPHPGSPQCHLATALIYAMSTIFMAIAYLIMFYILKA 209
 OY 164 QFENRHCQGGILQFEADTKAKESLFYR-----PSKE 197
 DB 210 KPNGQACSGGVAVKAVEAQTNRKLEDKRDVDPNVVIFPEKE 249

Search completed: October 26, 2002, 21:09:48
 Job time : 30 secs